



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/623,854
Source: OIPF
Date Processed by STIC: 8/1/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/623,854

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

see item 4 on Error summary
sheet

10/623,854 1

delete
□y"z-ñ·\□z
SEQUENCE LISTING

<110> NARA INSTITUTE OF SCIENCE AND TECHNOLOGY
<120> Multiple use of caffeine biosynthetic genes
<130> 19-023
<140>
<141>
<150> JP 2002-213655
<151> 2002-07-23
<160> 9
<170> Microsoft Word

These three
pages show
samples of
global errors

This file
could not be
processed -
invalid
format

<210> 1
<211> 372
<212> PRT
<213> ← insert this MANDATORY numeric identifier AND its response
<300>
<301> Ogawa, M., Herai, Y., Koizumi, N., Kusano, T., and Sano, H.
<302> 7-Methylxanthine Methyltransferase of Coffee Plants. Gene Isolation and Enzymatic Properties.
<303> Journal of Biological Chemistry
<304> 276
<305> 11
<306> 8213-8218
<307> 2001-03-16
<308> BAB39215
<309> 2000-09-11

Does Not Comply
Corrected Diskette Needed

<400> 1-
Met Glu Leu Gln Glu Val Leu Arg Met Asn Gly Gly Glu Gly
1 5 10
Asp Thr Ser Tyr Ala Lys Asn Ser Ala Tyr Asn Gln Leu Val
15 20 25
Leu Ala Lys Val Lys Pro Val Leu Glu Gln Cys Val Arg Glu
Leu Leu Arg Ala Asn Leu Pro Asn Ile Asn Lys Cys Ile Lys
Val Ala Asp Leu Gly Cys Ala Ser Gly Pro Asn Thr Leu Leu
Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys Val Gly Gln
Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile Phe
Leu Asn Asp Leu Phe Pro Asn Asp Phe Asn Ser Val Phe Lys
Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly
Arg Lys Ile Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser

Please
re-number
amino
acids

delete
14 invalid
28 numbering
42
56 Per 1.822 of
70 sequence rules,
84 number the
98 amino acids
112 under every 5
126 amino acids.
140
Do NOT use TAB codes
between amino acid
numbers. Use space
characters.

10/623,854 2

Phe Tyr Ser Arg Leu Phe Pro Glu Glu Ser Met His Phe Leu	154
His Ser Cys Tyr Cys Leu Gln Trp Leu Ser Gln Val Pro Ser	168
Gly Leu Val Thr Glu Leu Gly Ile Ser Thr Asn Lys Gly Ser	482
Ile Tyr Ser Ser Lys Ala Ser Arg Leu Pro Val Gln Lys Ala	196
Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg	210
Ile His Ser Glu Glu Leu Phe Ser His Gly Arg Met Leu Leu	224
Thr Cys Ile Cys Lys Gly Val Glu Leu Asp Ala Arg Asn Ala	238
Ile Asp Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu	252
Gly His Leu Glu Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro	266
Val Tyr Ile Pro Ser Ala Glu Glu Val Lys Cys Ile Val Glu	280
Glu Glu Gly Ser Phe Glu Ile Leu Tyr Leu Glu Thr Phe Lys	294
Val Leu Tyr Asp Ala Gly Phe Ser Ile Asp Asp Glu His Ile	308
Lys Ala Glu Tyr Val Ala Ser Ser Val Arg Ala Val Tyr Glu	322
Pro Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp	336
Ile Phe His Arg Phe Ala Lys His Ala Ala Lys Val Leu Pro	350
Leu Gly Lys Gly Phe Tyr Asn Asn Leu Ile Ile Ser Leu Ala	364
Lys Lys Pro Glu Lys Ser Asp Val	372

<210> 2
 <211> 1316
 <212> DNA
 <213> Coffea arabica

<220>
 <221> CDS
 <222> (45)□c(1163)

<300>
 <308> AB048793
 <309> 2000-09-11

<400> 2	
ctttggcagt cccaatttga tttatgtaca agtcctgcat atgaatggag	50
ctccaagaag tcttgccgat gaatggaggc gaaggcgata caagctacgc	100
caagaattca gcctacaatc aactggttct cgccaagggtg aaacctgtcc	150
ttgaacaatg cgtacgggaa ttgttgccggg ccaacttgcc caacatcaac	200

re-number

correctly

delete this (please delete ALL instances of this format marker throughout sequence listing)

10/623,854 3

<210> 4
 <211> ← *mandatory response needed*
 <212> PRT
 <213> Coffea arabica

<400> 4
 Met Glu Leu Gln Glu Val Leu His Met Asn Glu Gly Glu Gly 14
 Asp Thr Ser Tyr Ala Lys Asn Ala Ser Tyr Asn Leu Ala Leu 28
 Ala Lys Val Lys Pro Phe Leu Glu Gln Cys Ile Arg Glu Leu 42
 Leu Arg Ala Asn Leu Pro Asn Ile Asn Lys Cys Ile Lys Val 56
 Ala Asp Leu Gly Cys Ala Ser Gly Pro Asn Thr Leu Leu Thr 70
 Val Arg Asp Ile Val Gln Ser Ile Asp Lys Val Gly Gln Glu 84
 Glu Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile Phe Leu 98
 Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu 112
 Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg 126
 Lys Ile Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe 140
 Tyr Gly Arg Leu Phe Pro Glu Glu Ser Met His Phe Leu His 154
 Ser Cys Tyr Ser Val His Trp Leu Ser Gln Val Pro Ser Gly 168
 Leu Val Ile Glu Leu Gly Ile Gly Ala Asn Lys Gly Ser Ile 182
 Tyr Ser Ser Lys Ala Ser Arg Pro Pro Val Gln Lys Ala Tyr 196
 Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg Ile 210
 His Ser Lys Glu Leu Phe Ser Arg Gly Arg Met Leu Leu Thr 224
 Cys Ile Cys Lys Val Asp Glu Tyr Asp Glu Pro Asn Pro Leu 238
 Asp Leu Leu Asp Met Ala Ile Asn Asp Leu Ile Val Glu Gly 252
 His Leu Glu Glu Glu Lys Leu Ala Ser Phe Asn Leu Pro Phe 266
 Phe Thr Pro Ser Ala Glu Glu Val Lys Cys Ile Val Glu Glu 280
 Glu Gly Ser Phe Glu Ile Leu Tyr Leu Glu Thr Phe Lys Ala 294
 His Tyr Asp Ala Gly Phe Ser Ile Asp Asp Asp Tyr Pro Val 308
 Arg Ser His Phe Gln Val Tyr Gly Asp Glu His Ile Lys Ala 322
 Glu Tyr Val Ala Ser Leu Ile Arg Ser Val Tyr Glu Pro Ile 336
 Leu Ala Ser His Phe Gly Glu Ala Ile Met Pro Asp Leu Phe 350
 His Arg Leu Ala Lys His Ala Ala Lys Val Leu His Leu Gly 364

delete
re-number
correctly

*Please ensure that all nucleotides
 and amino acids are valid.*

**The types of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.**